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1 GGCCTGCCG CGCGGGGAGA AAGAACCGGC GCCCCAGCCCG GCGTCCCAG  
51 CAGCGCAGGG GAGGATCCCC GCGCAGTGAC CCGGGAGCCA CCACAGACTC  
101 TGGGAGGCTC GGCGGCTGGA GCAGCAGGCA GCTCCCCGCA GCTCCCGCG  
151 CTTCCAGGCA GCTCTCTGAG CCGTGCCAGA GGCCCCGGCCC GCCATTCCA  
201 GCCCCGAGCC ATGATGAAGA CTTTGTCCAG CGGGAACTGC ACGCTCAGTG  
251 TGCCCCGCAA AAACTCATAAC CCCATGGTGG TCCTGGGTGC CTCTCGGGTG  
301 GGCAAGAGCT CCATCGTGTGTC TCGCTTCCTC AATGGCCGCT TTGAGGACCA  
351 GTACACACCC ACCATCGAGG ACTTCCACCG TAAGGTATAC AACATCCGCG  
401 GCGACATGTA CCAGCTCGAC ATCCTGGATA CCTCTGGCAA CCACCCCTTC  
451 CCCGCCATGC GCAGGCTGTC CATCCTCACCA GGGGATGTC TCATCCTGGT  
501 GTTCAGCCTG GATAACCGGG AGTCCTTCGA TGAGGTCAAG CGCCCTCAGA  
551 AGCAGATCCT GGAGGTCAAG TCCTGCCTGA AGAACAAAGAC CAAGGGAGGCG  
601 GCGGAGCTGC CCATGGTCAT CTGTGGCAAC AAGAACGACC ACGGCAGAGCT  
651 GTGCCGCCAG GTGCCACCA CCGAGGCCGA GCTGCTGGTG TCGGGCGACG  
701 AGAACTCCGC CTACTTCGAG GTGCGGCCA AGAACAAACAC CAACGTGGAC  
751 GAGATGTCT ACAGTGTCTT CAGCATGGCC AAGCTGCCAC ACGAGATGAG  
801 CCCCGCCCTG CATCGCAAGA TCTCCGTGCA GTACGGTGAC GCCTTCCACC  
851 CCAGGCCCTT CTGCATGCGC CGCGTCAAGG AGATGGACGC CTATGGCATG  
901 GTCTCGCCCT TCGCCGCCG CCCCAGCGTC AACAGTGACC TCAAGTACAT  
951 CAAGGCCAAG GTCCCTCGGG AAGGCCAGGG CCGTGAGAGG GACAAGTGCA  
1001 CCATCCAGTG AGCGAGGGAT GCTGGGGCGG GGCTGGCCA GTGCCCTTCAG  
1051 GGAGGTGCC CCAGATGCCC ACTGTGCGCA TCTCCCCACC GAGGCCCCGG  
1101 CAGCAGCTTT GTTCACAGAC CTTAGGCACC AGACTGGAGG CCCCCGGCG  
1151 CTGGCCTCCG CACATTCGTC TGCCTCTCA CAGCTTCCCT GAGTCCGCTT  
1201 GTCCACAGCT CCTTGGTGGT TTCATCTCTT CTGTGGGAGG ACACATCTCT  
1251 GCAGCCTCAA GAGTTAGGCA GAGACTCAAG TTACACCTTC CTCTCCTGGG  
1301 GTTGAAGAA ATGTTGATGC CAGAGGGGT AGGATTGTC CGTCATATGG  
1351 AGCCTCTGG GACAAGCCTC AGGATAAAAA GGACACAGAA GGCCAGATGA  
1401 GAAAGGTCTC CTCTCTCTG GCATAAACACC CAGCTTGGTT TGGGTGGCAG  
1451 CTGGGAGAAC TTCTCTCCCA GCCCTGCAAC TCTTACGTC TGTTCAAGCT  
1501 GCCTCTGCAC CCCCTCCCAC CCCCAGCACA CACACAAGTT GCCCCCCCAGC  
1551 TGCGCCTGAC ATTGAGCCAG TGGACTCTGT GTCTGAAGGG GCGTGGCCA  
1601 CACCTCTTAG ACCACGCCCA CCACTTAGAC CACGCCACC TCCTGACCAC  
1651 GTTCTCTAGC CTCTCTCTCT AGGTCCCTCC GCCCGACAGT TGTGTTTGT  
1701 TGTGGTTGCA GCTGTTTCG TGTCTATAGT AGTAGTAGAA ATGAAATCA  
1751 TTGTACTGTA AAAGCCTAGT GACTCCCTCC TTGGCCAGGC CCTCACCCAG  
1801 TTCAGATCCA CGGCCTCCAC CCGGGACGCC TTCCCTCTCT GCTCCCAAAC  
1851 AGGGTTTCCG TGGCCTGTT GCAGCTAGAC ATTGACCTCC GCCATTGAGC  
1901 TCCACGGTT ACAGACAATT GCACAAGCGT GGGGTTGGCA GGCCAGGACT  
1951 GCTTTTTTTT AATGCTCCCA TTTCACAGAG GATACCCACCG AGACTCGGAG  
2001 GGGACACGAT GAGCACCCAGG CCCCCACCTTT GTCCCTCTAGC AAATTCAAGGG  
2051 TACAGCTCCA CCTAGAACCA GGCTGCCCTC TACTGTGCTC GTTCCTCAAG  
2101 CATTATTAAC GCACCTACTG GGTGCTGGGT TCACTGTGTC CTAGGAAACC  
2151 AAGAGGGTCC CCAGTCCTGG CCTCTGCCCG CCCCTGCTGC CCCACCACCT  
2201 TCTGCACACA CAGCGGTGGG GAGGCGGGGA GGAGCAGCTG GGACCCAGAA  
2251 CTGAGCTGG GAGGGATCCG ACAGAAAAGC TCAGGGCGGG TCTTCTCCTT  
2301 GTGCCGCCAG TTGGGCTATG CTGGGTACCA CCATGTACTC AGGCATGGTG  
2351 GGTTTGAAC CCATAAACCA AAGGCCCTTG TCATCAGCTC TTAACAAGTA  
2401 TATTTGTAT TTTAATCTCT CTAAACATAT TGAAGTTTA GGGCCCTAAG  
2451 GAACCTTAGT GATCTCTAT TGGGTCTTT TGAGGTTAG AGAGGGTAAG  
2501 TAACTCCTC CAGGTACAC ACAGCAAGCTG TGGGTGGCAG AAGCAAGCTA  
2551 GCGCTGGCA TTCAGTACAT ACCACGATGT GCTCCCTCTC TTGATGCTTG  
2601 GCCCCCTGGG CCTTCAGGGC TTTGGGACAT CTTGTCTCTA ACCCTCTCCC  
2651 TAGATCAGTC TGTGAGGGTC CCTGTAGATA TTGTGTACAC CATGCCCATG  
2701 TATATACAAG TACACACAGA TGTACACACA GATGTACACA TGCTCCAGCC  
2751 CCAGCTCTGC ATACCTGCAC CTGCACCCCA GCCTTGGGCC CTGCTCTGGT  
2801 CTGTGCTCAA AGCAGCAGCT CCAACCCCTGC CTCTGTCCCC TTCCCCACCC  
2851 ACTGCCTGAG CCTTCTGAGC AGACCAGGTA CCTTGGCTGC ACCGGTGTGT  
2901 GGGCCGCTCT CACCCAGGCA CAGCCCCGCC ACCATGGATC TCCGTGTACA  
2951 CTATCAATAA AAGTGGTTT GTTACAAAAA AAAAAAAA AAAAAAAA AAAAAAAA  
3001 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAA  
3051 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA

FIGURE 1, page 1 of 3

**FEATURES:**

5'UTR: 1-210  
Start Codon: 211  
Stop Codon: 1009  
3'UTR: 1012

**5' UTR ANALYSIS:**

Query=cDNA clone  
Sbjct: genomic sequence

**5' UTR Exon 1, non-coding**

Score = 58.0 bits (29), Expect = 2e-10  
Identities = 29/29 (100%)  
Strand = Plus / Plus

Query: 1 ggcgtcgccgcgccccggggagaaagaagccg 29  
|||||||||||||||||||||||||  
Sbjct: 1535 ggcgtcgccgcgccccggggagaaagaagccg 1563

**5' UTR Exon 2, non-coding**

Score = 349 bits (176), Expect = 3e-98  
Identities = 176/176 (100%)  
Strand = Plus / Plus

Query: 26 gccgcgcccagcccggtcccgagcagcgcagggaggatccccgcgcagtgaccggg 85  
|||||||||||||||||||||||||  
Sbjct: 2001 gccgcgcccagcccggtcccgagcagcgcagggaggatccccgcgcagtgaccggg 2060

Query: 86 agccaccacagactctgggaggctcgccggctggagcagcaggcagctcccgccagtc 145  
|||||||||||||||||||||||||  
Sbjct: 2061 agccaccacagactctgggaggctcgccggctggagcagcaggcagctcccgccagtc 2120

Query: 146 cggcgttccaggcagctcttgatggccgtgccagaggccggccgcattccag 201  
|||||||||||||||||||||||||  
Sbjct: 2121 cggcgttccaggcagctcttgatggccgtgccagaggccggccgcattccag 2176

Score = 563 bits (284), Expect = e-162  
Identities = 284/284 (100%)  
Strand = Plus / Plus

**5' UTR Exon 3, Protein coding region begins at nucleotide 211**

Query: 199 cagccccgagccatgtgaagactttgtccagcggaaactgcacgctcagtgtgcccgcc 258  
|||||||||||||||||||||||||  
Sbjct: 7474 cagccccgagccatgtgaagactttgtccagcggaaactgcacgctcagtgtgcccgcc 7533

**Homologous proteins:****Top BLAST Hits**

	Score	E
CRA 18000005194969 /altid=gi 10047088 /def=ref NP_055125.1  sim...	538	e-152
CRA 18000005238449 /altid=gi 5059122 /def=gb AAD38928.1 AF13440...	512	e-144
CRA 332000009620725 /altid=gi 8118457 /def=gb AAF72997.1 AF2620...	342	2e-93
CRA 18000005232775 /altid=gi 7706359 /def=ref NP_057168.1  ras-...	342	2e-93
CRA 8700000006130 /altid=gi 7230768 /def=gb AAF43090.1 AF23915...	342	3e-93
CRA 18000005090459 /altid=gi 6677673 /def=ref NP_033052.1  RAS,...	341	6e-93
CRA 89000000197633 /altid=gi 7295299 /def=gb AAF50620.1  (AE003...	228	8e-59
CRA 105000014645240 /altid=gi 10503969 /def=gb AAG17979.1 AF177...	214	1e-54

BLAST dbEST hits:

gi 9345313 /dataset=dbest /taxon=960...	880	0.0
gi 9335874 /dataset=dbest /taxon=960...	846	0.0
gi 10143211 /dataset=dbest /taxon=96...	821	0.0
gi 9335309 /dataset=dbest /taxon=960...	813	0.0
gi 9150610 /dataset=dbest /taxon=9606...	662	0.0
gi 10144589 /dataset=dbest /taxon=96...	617	e-174
gi 9333908 /dataset=dbest /taxon=960...	599	e-169

**EXPRESSION INFORMATION FOR MODULATORY USE:**

library source:

Expression information from BLAST dbEST hits:

gi 9345313 Placenta choriocarcinoma
gi 9335874 Uterus endometrium adenocarcinoma
gi 10143211 Skin melanotic melanoma
gi 9335309 Uterus endometrium adenocarcinoma
gi 9150610 Skin melanotic melanoma
gi 10144589 Skin melanotic melanoma
gi 9333908 Uterus endometrium adenocarcinoma

Expression information from PCR-based tissue screening panels:

Human fetal whole brain

1 MMKTLSSGNC TLSVPAKNSY RMVVLGASRV GKSSIVSRFL NGRFEDQYTP  
51 TIEDFHRKVY NIRGDMYQLD ILDTSGNHPF PAMRRLSILT GDVFILVFSL  
101 DNRESFDEVK RLQKQILEVK SCLKNKTKEA AELPMVICGN KNDHGEELCRO  
151 VPTTEAELLV SGDENSAYFE VSAKKNTNVD EMFYVLFSMA KLPHEMSPAL  
201 HRKISVQYGD AFHPPRFICMR RVKEMDAYGM VSPFARRPSV NSDLKYIKAK  
251 VLREGQARER DKCTIQ

**FEATURES:**

**Functional domains and key regions:**

[1] PDOC00001 PS00001 ASN\_GLYCOSYLATION  
N-glycosylation site

Number of matches: 2  
1 9-12 NCTL  
2 125-128 NKTK

[2] PDOC00004 PS00004 CAMP\_PHOSPHO\_SITE  
cAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 4  
1 84-87 RRLS  
2 174-177 KKNT  
3 202-205 RKIS  
4 236-239 RRPS

[3] PDOC00005 PS00005 PKC\_PHOSPHO\_SITE  
Protein kinase C phosphorylation site

Number of matches: 2  
1 19-21 SYR  
2 172-174 SAK

[4] PDOC00006 PS00006 CK2\_PHOSPHO\_SITE  
Casein kinase II phosphorylation site

Number of matches: 5  
1 51-54 TIED  
2 105-108 SFDE  
3 154-157 TEAE  
4 161-164 SGDE  
5 177-180 TNVD

[5] PDOC00007 PS00007 TYR\_PHOSPHO\_SITE  
Tyrosine kinase phosphorylation site

220-228 RRVKEMDAY

[6] PDOC00266 PS00294 PRENYLATION  
Prenyl group binding site (CAAX box)

263-266 CTIQ

[7] PDOC00016 PS00016 RGD  
Cell attachment sequence

63-65 RGD

[8] PDOC00017 PS00017 ATP\_GTP\_A  
ATP/GTP-binding site motif A (P-loop)

26-33 GASRVGKS

**BLAST Alignment to Top Hit:**

>CRA|18000005194969 /altid=gi|10047088 /def=ref|NP\_055125.1| similar  
to mouse Ras, dexamethasone-induced 1; tumor endothelial  
marker 2 [Homo sapiens] /org=Homo sapiens /taxon=9606  
/dataset=nraa /length=278  
Length = 278

Score = 538 bits (1372), Expect = e-152  
Identities = 265/266 (99%), Positives = 265/266 (99%)

Query: 1 MMKTLSSGNCTLSPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60  
MMKTLSSGNCTLSPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY  
Sbjct: 13 MMKTLSSGNCTLSPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 72  
  
Query: 61 NIRGDMYQLDILDTSGNHFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 120  
NIRGDMYQLDILDTSGNHFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK  
Sbjct: 73 NIRGDMYQLDILDTSGNHFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 132  
  
Query: 121 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENSAYFEVSAKKNTNVD 180  
SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDEN AYFEVSAKKNTNVD  
Sbjct: 133 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENCAYFEVSAKKNTNVD 192  
  
Query: 181 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 240  
EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV  
Sbjct: 193 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 252  
  
Query: 241 NSDLKYIKAKVLREGQARERDKCTIQ 266  
NSDLKYIKAKVLREGQARERDKCTIQ  
Sbjct: 253 NSDLKYIKAKVLREGQARERDKCTIQ 278

Complete Amino Acid Sequence of gi|10047088 /def=ref|NP\_055125.1| similar  
to mouse Ras, dexamethasone-induced 1; tumor endothelial  
marker 2 [Homo sapiens] /org=Homo sapiens /taxon=9606  
/dataset=nraa /length=278  
Length = 278

**NOTE: UNDERLINED RESIDUES NOT PRESENT IN THE PROTEIN OF THE PRESENT INVENTION**

1 mpasllqp rammktlssg nctlsvpakn syrmvvlgas rvvkssivsr flngrfedqy  
61 tptiedfhrk vynirgdmyq ldildtsgnh pfpmrrlsi ltgdvfifvf sldnresfde  
121 vkrlqkqile vksclknktk eaaelpmvic gnkndhgeli rqvptteael lvsgdencay  
181 fevsakkntn vdemfyvlfs maklphemsp alhrkisvqy gdafhprpf mrrvkemday  
241 gmvspfarrp svnsdlkyik akvlregqar erdkctiq

>CRA|18000005238449 /altid=gi|5059122 /def=gb|AAD38928.1|AF134409\_1  
(AF134409) Rhes protein [Rattus norvegicus] /org=Rattus  
norvegicus /taxon=10116 /dataset=nraa /length=266  
Length = 266

Score = 512 bits (1304), Expect = e-144  
Identities = 252/266 (94%), Positives = 256/266 (95%)

Query: 1 MMKTLSSGNCTLSPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60  
MMKTLSSGNCTL+VPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY  
Sbjct: 1 MMKTLSSGNCTLNVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60  
  
Query: 61 NIRGDMYQLDILDTSGNHFPAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 120  
NI GDMYQLDILDTSGNHFPAMRRLSILTGDVFILVFSLD+RESFDEVKRLQKQILEVK  
Sbjct: 61 NIHGDMYQLDILDTSGNHFPAMRRLSILTGDVFILVFSLDSRESFDEVKRLQKQILEVK 120  
  
Query: 121 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENSAYFEVSAKKNTNVD 180  
SCLKNKTKEAAELPMVICGNKNDH ELCRQVP EAELLVSGDEN AYFEVSAKKNTNV+  
Sbjct: 121 SCLKNKTKEAAELPMVICGNKNDHSELCRQVPAMEAELLVSGDENCAYFEVSAKKNTNV 180

Query: 181 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRFCMRRVKEMDAYGMVSPFARRPSV 240  
EMFYVLFSMAKLPHEMSPALH KISVQYGDAFHPRFCMRR K AYGMVSPFARRPSV  
Sbjct: 181 EMFYVLFSMAKLPHEMSPALHHKISVQYGDAFHPRFCMRRKVAGAYGMVSPFARRPSV 240

Query: 241 NSDLKYIKAKVLREGQARERDKCTIQ 266  
NSDLKYIKAKVLREGQARERDKC+IQ  
Sbjct: 241 NSDLKYIKAKVLREGQARERDKCSIQ 266

**Hmmmer search results (Pfam):**

Model	Description	Score	E-value	N
PF00071	Ras family	126.2	2.8e-36	1
CE00060	rab_ras_like	20.7	0.00013	2

**Parsed for domains:**

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00060	1/2	22	52 ..	26	56 ..	16.9	0.0014
CE00060	2/2	162	183 ..	159	181 ..	3.3	7.5
PF00071	1/1	21	186 ..	1	169 [.	126.2	2.8e-36

1 CTCTCTGACT CTTTGCCTCC TCTCTGACTC CCTGCCCTCT CTCTCTGTCT  
 51 CCCTGCCCTCC TCTGTCTGAC TCCCTGCCCTC CCCTCTCTGT CTCACTGCCCT  
 101 CCTCTCTCTG ACTCTCTGCC TCCCTCTCTGT GACTCCCTGC CTCCTCTCTC  
 151 TGATTCCCTG CCTCTTTGAC CCTCTGCCCTC CTCTCTTTGA CTCCCTGCCCT  
 201 CCTCTCTCCG ATTCTCTGCG TCTTTGACTC CCTGCCCTCT CTCTCTGACT  
 251 CCCTGAAGCT CATTCACTGCA TTGCTATCAA CTCGTCTGTA CCAAGCTCTA  
 301 GGCTGGAGGC TGGGCAGGGC AATGATGGAG ACAAAATACTG TCCCTGGGAG  
 351 CTTCTGGCCC CTTTCCCCATC CTGTTTAGAC AGAAAGTGACC GCCAGCAGAG  
 401 TCAAGCTGTC TGCAGAAGGA CTTGGGGAGG GGGCTGTCAT GGGGTAGGGC  
 451 TTCTTCCCCC CCATCTCTGC TGAAGGGCCA GGCTGGCTGA GACAGCCCCG  
 501 GCAGAGACTG AGAAGGGCTC CTCGCTGTGG TCTGGCAGCC CCCTCTCCAC  
 551 CCTCCTCTCT CTCATTTCT GCCTCCCACA CGTATGCCCT GGGCACCTCA  
 601 TCAGGGCTGC CCTAGGGGAG GGCCCTCCTT GGCACAGCCC CTGGGCCAGT  
 651 CAGGTGGTTG AGGCTGAGGA GAGAAGGTCC CAGAGTGGGG CTTCAGGCAA  
 701 ACCCAAAGAC AGAGCCCTT GCCATTGAT GAATGCACAG ACCCTTTATT  
 751 GAGCCCCCTGC TCTGTTCATG GCATGGCAGT TTTGTGGGAT AAATTCAAAG  
 801 ACAGCTTAG GTGGGAGCTG GGTGGGGGAT GTGGGGTCT TAGGCTTGA  
 851 CTACTACCCA GCCTCCCTTG TTAACCAAGT AGCTAGTCAC GTAGCCTTCT  
 901 GAGCTCGGGG CAGACCACCT GGGATCAAAAC CTCTCTCTG CTGGTTACTG  
 951 GCTGTGCAAC TGTAAGCAAG TAATTTAAC TCTCTGTGCC TCAGTTCCCT  
 1001 CATCTGAAA TTGGAGAATA ACACCCACCTG CTTCTGGGG TTATGAAGGG  
 1051 AGAAATAGGT TAACATGTGT GCAGCACTTA GAACACTCTG GCATATTTTA  
 1101 GCTGCAAAT GAATGCCAGC TATGATTATT TCTATACCTA GTCCGGGGCT  
 1151 TGGCACACTG CATGGCTCA AGTGGCAGCA GTTGTGCGTCC TTGTGGCTCC  
 1201 AGGCCTGGGG TCCGGCGTGT GCTGAGCTGG CTTATTGTGC ACCTCCCTT  
 1251 GTGATTCACTT CATCGAAGTC ACATTAGTAG CTTAGAACTG ACCGTAGTGG  
 1301 GAGCATTAC GCCATGGAAA TTGGCAATAG GGCTTTAAC AAAGGTATT  
 1351 TTGAGAGCCG GTTTCCTGCA CAGAGGCTGG TAGTTGGGCA GGGTGAGCAG  
 1401 ATCCAGATGT GTGCCAGGGG CTCGCACGCA GGCAATCTCT CCACCTCCAG  
 1451 TGGCCATCTC AGACCTTAGC TTCATGATAG CCAGGAAGCG ATGGTGTGG  
 1501 AAAGGCCCTT GGGTCAATGG GCGAGGCAGT CAAGGAACCC GACTTGGGGC  
 1551 ATCCCTGGGT GGGGACCGAG TTTGGGCACA TACAGCCCTT TGTGTGAATT  
 1601 TAAAAAACAGT GCCTTTCCCT CTACACAAGA TGCCCTTCTG TCTGGGATAC  
 1651 AGCCCCCACC TCTGGGATGC AGCCCCCACC TGCCCACCCA GCCATGCGCC  
 1701 TTGTGCAGTA TCCAACCTGC ACAACCTGTG GCAGCCTGTG GAAGACCGAG  
 1751 GGGATTGATA TTTCAGCAGG CCTGTGCCA TTTGCAGTTC AGGGGCTGGA  
 1801 AAGCTCTCCT CTGGAGAGGG GAGGGAITCC TGCAAGGGTG AGGAGATCAG  
 1851 AGAGGCCTTC AGAGAGCAGG TGGAACCTGA GCCAGACCC GAAACATAAG  
 1901 GGGAAAGAGGG TGTCTGCAAG AGGGGTGGCA TGAGCAAAGG AGTGGAGGCT  
 1951 GATCTCAGCA GAGCTCAAAC TGACGAGGGT GACTGGGTC AGGGGTTCTG  
 2001 GGGGGGGGAT TCTGGTGGGC GCTAAGGTAG GAAAGGAGGG AGGGCTGGG  
 2051 TGTGAAGAGC CTTTGGGTG AGCCTGGTGG AGCCTGCGGG TTTGCTTATA  
 2101 CAAGAGCTT GATCCATGTG GGCCTCTTTC ATGAGGTCAA GAGGCTCCCA  
 2151 TAGAAAGCTC TGAGTTGCC CCAGAACCAT AACCCCTTGGA GATGGGAGGG  
 2201 AAGCTTGAGC CAGCCATGGG TCGTTCCCCA TTCCACATCC TCTACTCCGG  
 2251 GCCTCTGGGT CTCCTGGAGG CAAGTAAACA CCTAGGGCCT GGGAGGCAA  
 2301 AATATCCGGG CAGGTCACTGG AGCGGAGGGA GCCGCCAGA TGCGAGGCAC  
 2351 AGGTCTAAAG GTGGGTCTC CTGAGGTGGC TGCAGGAGCA ACCCCAGGCA  
 2401 TTGGGCTTGG AGCATGCGGT GTGGACATAG CCTTCCCTTC TTCCCAGGAG  
 2451 GGCTGAATGG CCAACAGAAC ACCCCCTGCC CCAGGCTTAA GAAATGCATG  
 2501 CTAGTGCCTT CCCCATGTCT TATCCTAGAA TCACAGGCTC CGGGAAAGCC  
 2551 AGATGGATGA ACCAGGGAAA GAACGGATTC TCACCATAGA TACCATTTTT  
 2601 GAGATTTCAC CATGTGCTGA GCCCTTTGCA ACAACTCTAT GAATTGGGCT  
 2651 CATTTCGAG ATGAGAAAAG TGACTTCTAG AGAGGTTAAG CTACTAGGCC  
 2701 AAGATCAGTA GCTAGAGGGCA AGGCAAGGAT TCAAATCCCA GGAGTCCGGT  
 2751 GCTTGCATAA ATGAAAGGAT GAATGAACGG ATATTGAGTG AGTGAAGTGG  
 2801 TGAAGGAAGG AGTAAAGGAG AGGGCATGAA TGAATGAGAG GGTAGAACTC  
 2851 CAAGACCCCT TAGAACCTCG TCTGATGTTTC CCATTTACA GACAGAAAAC  
 2901 TGAGTCCTAG ACAGAGGCC AGAGGAGGGC AAGAGGTGGT GGGGCCAGGT  
 2951 CGGGGGGGCC CTGATGCCCTG CTTCTCTCGC TTTGTGCGAG CCCCGAGCCA  
 3001 TGATGAAGAC TTTGTCCAGC GGGAACTGCA CGCTCAGTGT GCCCGCCAAA  
 3051 AACTCATACC GCATGGTGGT GCTGGGTGCC TCTCGGGTGG GCAAGAGCTC  
 3101 CATCGTGTCT CGCTTCCCTCA ATGGCCGCTT TGAGGACCAG TACACACCCA

FIGURE 3, page 1 of 6

0 0 0 0 0 0 0 0 0 0

3151 CCATCGAGGA CTTCCACCCT AAGGTATAACA ACATCCGGG CGACATGTAC  
3201 CAGCTCGACA TCCTGGATAC CTCTGGCAAC CACCCCTTCC CGGCCATGCG  
3251 CAGGCTGTCC ATCCTCACAG GTGAGGCCA CTGGTGCCTG GGCTGGGCG  
3301 GCAGGGCCAG GGCATGGGTG CGGAGTGTGC TGGGCACTTG GCAGTTGCA  
3351 TAGACTTGCA TAGCCATCGT CTGAGACAGG CGTCATCCCT GCACAATGAG  
3401 GCTCAGAGAG GTTTGCCAT GTGCTGGAAA TAGTGTGAA GTGGGGGGCC  
3451 CCGATTCCAT TCTGTTAGAC TCCAGATCGA TTACTCATGG CTGTCGGGGC  
3501 CGCCTTCCAG ATCAGGAGCT GATACCAGCA TGCCCCAGGG ATATTCCCTT  
3551 CTAGGGAAACA GAATGATGCC CTGGCTGCTG CTTCCTCTC CGGAAAGATG  
3601 ACCCACCCAGA GCTCCAGGGC CCAAGGTAG CTCACGGGGC TCAGGTCTCC  
3651 CACACCCAG GCCTTGCCA CCTCCTAGAG AGGTAAGGGC AGGACCCAGG  
3701 CAGTGATCAC CAAAGGGAAAG GGGGCTTGGT CATGGTCATA GTGATGGTGA  
3751 TGGCACTAGC TGACACTTAT CAGAAGCTAT GGGCCTGGCC CTGTTCTTAG  
3801 AGCTTGGCAT GTAGTTTTT TTGAAACAGA GTCTCGCTCT GTCACCCAGG  
3851 CTGGAGTGC A GTGGCGCGAT CTCGGCTCAC TGCAACCTCT GCCTCCGGG  
3901 TTCAAGCGAT TCTCCTGCCT CAGTCCCCCA AGTAGCTGGG ACTACAGGC  
3951 CGTGCCACCA TGCCCGGCTA ATTTTTGTA TTTTACTAG AGACGGGATT  
4001 TCACCATGTT AGCCAGGATG GTCTCGATCT CCTGACCTCG TGATCTGCCT  
4051 ACCTCAGCCT CCCAAAGTGC TGAGATTACA GGCAGTCAGCC ACCGCGGCCA  
4101 GCCAGCATGT AGTTATTAA CCCTCACAGT AAATAGTTAT TCATTCCCTT  
4151 TTTACAGGTG GGGAAACTGA AGCCCCAGAGA GGTAAAGTAA CTCACTCCAG  
4201 TGGTAGCACA GCTCGTAAAG GCAGTCTGCT TTTGTGCTTT CAGACAAAGC  
4251 CATACCACAG CCTCTCAGCC CTGCTGGGAA GGGTGAAGGAG GGACAGGGAG  
4301 GTTGGGGGAA AGAAGGGGTG AGTGGAGCTG AGGGGCTGTG CCCTTGTGTTA  
4351 CACTGCATTA GCATGGTAGC TAAGAGGACA AGCCCCGGAC CCAGCACCTG  
4401 GGTGTGAGCC CTGGTTCCGC TGCTTCCTGG CTTTGTACCT CGAGGCAAGG  
4451 GATTTTATCT CCTTGTGTCT CAGCACTCTC ATCTGTAAGA CTGACCCACA  
4501 TCAACACTCA TCCTAAAGGG ACTGTGAGAC TTAAATGAAT GAATATATGT  
4551 AAGGCGCTTG GTGAGCAGAT AGTAAATGCA CAATAATCC CCAAGTCTTC  
4601 TGTTGAGTC GCATTGCAA GTGGGCTGTG TACGGTTAC ACCATCATTT  
4651 CCCAAAGTCAC GCCCCCTGAAG TTGCTGAGCA GGGATAAGGG AAGGAGTGA  
4701 CAGGCAACTC TCTAGGCATC ATTCAAGATAA CCCCCCAACT GAGGTACTTC  
4751 TATAAGGAGA AACCCATGCC ACTCCCAGCC CTGCTGCCGC CTTGAGGCCA  
4801 AGACTGAGGC TGCGGGGTGG CCCCTCCCTG AGTGTGTTCT CTTCCAGGCT  
4851 GGCTTTCCG AGCATCTGAC CCAGACAGCA GTCAAGTTCT CCGCTCCACC  
4901 CCGAGTTTG GAGAAGGGC ATGTAGATAG GAGAGCCCTG GGTGACCTG  
4951 TGTTCGAATC CTTGCTGGC CTCTTGGCTT AAATGTGTA CCAGAGGCAC  
5001 ATGCATCCTG TCTGAGTC CAGCCCTCCCA GCCACACAGT GGGCTTAACC  
5051 TCATACCCCG CAGGGAGGCT GTGAGGACTG CAAGAAGGCT TGTGGCGGGA  
5101 GCTTCCAGCA CGTGACGGGT ATTGCAATTGG TGTCAGCTCC CCCAGCCTTG  
5151 GGGAGGGGAC TGGGTACCCG CTGCAATGAA TAAGGCTAAT GACAGAGGGA  
5201 AGGAGAGGGG AGATGTAGAG AGGAAGCACA TGCAATTGTT CAGCATTAAAT  
5251 TTTCAGTGAC ACAAGTAATA CCCAACACCA CCCTCTGCA AACGCTACAG  
5301 ATAAAGCTAA TGCCCTTTG ACCCATGTCC CCAATCCCAG GCTCCTGCC  
5351 CTGCCCCGGG GGTGGCCACC CTGGCAGTCT GGCATGGAGC CTTCCGGGGC  
5401 TCCGTGACT CACCGGCATT CGTATTTGTA TCCCCACAAT GGAGAGTATT  
5451 TTTGTCTGTC TCTTTTTAT GGCGCATATC ATTCTGAGCA CAGCTGTCTG  
5501 ATGCTTGTGTT TTTTTCAACA CACCAACCCG TGCTCATTT TCCAACCTGG  
5551 TGGAACTCTA TTTTTCAAC CTCATTTC TGCTGCTCAG GAAATTCTGA  
5601 AAGCCATTAA TTCCACTGCC AGCTCTTCTT CCAGCTGCCA GACGGGGCGA  
5651 TCTCTGATGC TTGGCATCGC AGTCTCGCAT TTGAATATGT CAAGGCCACG  
5701 AGTCTCAGG GGGCCGGAT TAGCCTAACG GGATGGGGTT TGGCAGCCCA  
5751 AGCAGGAAGA GTTGCCTAACG TGACGCTGCC TCGCAAGTGC CTTTCAGAAG  
5801 AGCCCCACACT GCAGTTCCCT CCATCACCTC CCATCCATTG AGGCTTCCCT  
5851 GGTTAACACT GACTGTGTGC CAGGCCCTGG GGAGACCAGG ACGAGTGGGT  
5901 GATGGAACCC TTCTCTGTGC CCGAGCTGTT TGGGACACAC CTTTGATCTG  
5951 GACACCATTG TGAATGTGCC ATGTGCCATT AAATGGGGTT AAATGATGTG  
6001 CTCTGGGGGT GCAGAGGAAG GTGGCAGCCA TTCTGCCAGA AGCTGGAACCT  
6051 GGTTGCTTCT CTTCTCAAGA ATTTGGGCCA ATTGCTGATT CCTCTGGGGC  
6101 TCAGTTCCCT CATCTGTGAG ACAGGGATCT TGTCACACCA CAAGGCTATC  
6151 AAGAGTTTGA GCAAAAGTGG TTGGACGCCAG TGGCTCATGC CTGTAATCCC  
6201 AGCTTTGG GAGGCCGAGG TGGGACGCCAG TCTTGAGGTC AGGAGTTCAA  
6251 GACCAGCCTG GCTAACACAG TGAAACACCG TCTCTACTAA AAAATACAAA

FIGURE 3, page 2 of 6

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6301 AAATTAGCCA GGTGTGGTGA TGGGCACCTG TAATCCAGT TACTCGGGAG  
6351 GCTGAGGCAG GAGAATCTCT TGAACCCAGG AGGTGGAGGT TGCAGTGAGC  
6401 TGAGATCTTG CCATTGCATT CCAGGCTGGG CAACAAGAGT GAAACTCTGT  
6451 CTCAGAAAAT AAATAAATAA ATAATATAAA AATAGCTAGG CATGGTGACA  
6501 GGCGCCTGTA ATCCCAGCTG CTCCAGAGGC TGAGGCAGGA GAATCGCTTA  
6551 AACCCAGGAG GTGGAAGTTG CAGTGAGCCA AGATCACACC ACTGCACTCC  
6601 AGCCTGGGCC ACAGAGAAAG ACTCCATCTC AAAAAAAA AAAAAAAA  
6651 AAAAGTTTA AGCAAAAGTG AGGAAGGTGC TTATTAAG CTGGAAATCA  
6701 GGATGGAGGT ACCAGTCCAG ACAGCCTCCC CACCACCCA CCGTCTCCAC  
6751 AGCAGCCCCCT GTTTCAGATT CACAAGCCTG CCTTGAGTGA TGCAGTGAGT  
6801 TATCCTGGAG GCAGTGTGGG CCTTGGAGGC CAGCACTCAC TTTTCATCC  
6851 TATGATTAT TTGAGAAGCA GAGAGCACCT ACCGGGTGCC AGGAACGAGC  
6901 TAGGTGAGAA CAGAATCAGG TAGAAATCTC AGCCTAGCCA CACGGAGCT  
6951 GTGTGATCTT GGGCAGGCTG CATAACCTTT CTGAGCCTCA GTTTGCTCAC  
7001 CTGTAATGCA AAGGTAACAA AATCTTGACA GAGGCATAGT GAGGAATCAA  
7051 GAGAACAAACG GGCCTGGAGC ATACACCCAG TGCTTAGCCC CCAGTAGGCC  
7101 CTCACTCTCA TCATTACTGA CACCTGAGGT CACTGAGCAT GTGCCACTGT  
7151 CCATTCACTTA TCTTGATCAA CTCCCCAAAT CATCCTGCAA GGTAAATATT  
7201 CATCTTCATG AAACAGACAG AGAAACTGAG GTTACAGAGG TTTCTGTGATC  
7251 TGCCCAAGTC TGCTGGCAGC TAAGCGGATG AGGCCAGATG CAAACTAGGC  
7301 ATTGAGCAAG ACAGGCAGGA CCCCTGCTCT CATAGAAATG ATTTTTATTA  
7351 TTATCTGAAC ACAGTCCACA CAAGTGACCT ACCCCTCTCC AGCCCTGCAA  
7401 AGAAATGTGA AGTGAGTTAA CTGTATTTGA ACCAAGTGGT CCACGTGTTA  
7451 GCTATGCGAC TGTGAACAGG GGCTTCACCC CCCTCAGCCT CAGTTCTGT  
7501 TCCTGGAAAA TAATCGCAGG GAGAATAATC GCAGCTACCC CGAAGAGTCG  
7551 CTGTGTAGGT TAAAGCAGTT ATGCCGCATA ACTGCTTCAG GCCACCTGTG  
7601 ACTCCCAGCT CTTAGGGCTG ATGTTCTGTG GCCAGAGGAG GGCAGGGGTT  
7651 GCAGCTGGCC GGTGAACTCA CTACCTGGGC TCTCTCCCTG CAGGGGATGT  
7701 CTTCATCCTG GTGTCAGCC TGGATAACCG GGAGTCCTTC GATGAGGTCA  
7751 AGCGCCTCA GAAGCAGATC CTGGAGGTCA AGTCCTGCCT GAAGAACAAAG  
7801 ACCAAGGGAGG CGGGGGAGCT GCCCCATGTC ATCTGTGGCA ACAAGAACGA  
7851 CCACGGCGAG CTGTGCCGCC AGGTGCCAC CACCGAGGCC GAGCTGCTGG  
7901 TGTCGGGCGA CGAGAACTGC GCCTACTTCG AGGTGTCGGC CAAGAAGAAC  
7951 ACCAACGTGG ACGAGATGTT CTACGTGTC TTCAGCATGG CCAAGCTGCC  
8001 ACACGAGATG AGCCCCGCCA TGCTATGCCAA GATCTCCGTG CAGTACGGTG  
8051 ACGCCTTCCA CCCCCAGGCC TTCTGCATGC GCCCGCTCAA GGAGATGGAC  
8101 GCCTATGGCA TGGTCTCGCC CTTCGCCCGC CGCCCCAGCG TCAACAGTGA  
8151 CCTCAAGTAC ATCAAGGCCA AGGTCCCTCG GGAAGGCCAG GCCCGTGAGA  
8201 GGGACAAGTG CACCATCCAG TGAGCGAGGG ATGCTGGGAG GGGGCTTGGC  
8251 CAGTGCCTTC AGGGAGGTGG CCCCAGATGC CCACTGTGCG CATCTCCCCA  
8301 CCGAGGCCCG GGCAGCAGTC TTGTTCACAG ACCTTAGGCA CCAGACTGG  
8351 GGCCCCCGGG CGCTGGCCTC CGCACATTG TCTGCCCTCT CACAGCTTTC  
8401 CTGAGTCCGC TTGTCCACAG CTCCCTGGTG GTTTCATCTC CTCTGTGGG  
8451 GGACACATCT CTGCAGCCTC AAGAGTTAGG CAGAGACTCA AGTTACACCT  
8501 TCCCTCCCTG GGGTGGAAAG AAATGTTGAT GCCAGAGGG TGAGGATTGC  
8551 TGCCTCATAT GGAGCCTCTT GGGACAAGCC TCAGGATGAA AAGGACACAG  
8601 AAGGCCAGAT GAGAAAGTC TCCTCTCTCC TGGCATAACA CCCAGCTTGG  
8651 TTTGGGTGGC AGCTGGAGA ACTTCTCTCC CAGCCCTGCA ACTCTTACGC  
8701 TCTGGTTCAAG CTGCCTCTGC ACCCCCCTCCC ACCCCCCAGCA CACACACAAG  
8751 TTGGCCCCCA GCTGCGCCTG ACATTGAGCC AGTGGACTCT GTGTCTGAAG  
8801 GGGCGTGGC CACACCTCT AGACCACGCC CACCACTTAG ACCACGCCA  
8851 CCTCCTGACC GCGTTCTCA GCCTCCTCTC CTAGGTCCT CCGCCCGACA  
8901 GTTGTGCTTT GTTGTGGTTG CAGCTGTTT CGTGTCTGT ATAGTAGTAG  
8951 AAATGGAAAT CATTGACTG TAAAAGCTA GTGACTCCCT CCTTGGCCAG  
9001 GCCCTCACCC AGTCAGATC CACGGCTCC ACCCGGGACG CCTTCCCT  
9051 CTGCTCCCAA ACAGGGTTTC CGTGGCCTGT TTGCAGCTAG ACATTGACT  
9101 CCGCCATTGA GCTCCACGGT TTACAGACAA TTGCACAAGC GTGGGGTGG  
9151 CAGGCCAGGA CTGCTTTTT TTAATGCTCC CATTTCACAG AGGATACAC  
9201 CGAGACTCGG AGGGGACACG ATGAGCACCA GGCCCCACCT TTGTCCTA  
9251 GCAAATTCAAG GGTACAGCTC CACCTAGAAC CAGGCTGCC TCTACTGTGC  
9301 TCGTTCCCTCA AGCATTATT AAGCACCTAC TGGGTGCTGG GTTCAGTGT  
9351 TCCTAGGAAA CCAAGAGGGT CCCCAGTCTT GGCCTCTGCC CGCCCCCTGCT  
9401 GCCCCACCAAC CTTCTGCACA CACAGCGGTG GGGAGGCAGG GAGGAGCAGC

FIGURE 3, page 3 of 6

9451 TGGGACCCAG AACTGAGCCT GGGAGGGATC CGACAGAAAAA GCTCAGGGCG  
 9501 GGTCTTCCTCC TTGTGCCCGG GATTGGGCTA TGCTGGGTAC CACCATGTAC  
 9551 TCAGGCATGG TGGGTTTGA ACCCATAAAC CAAAGGCCCT TGTCACTCAGC  
 9601 TCTTAACAAG TATATTTGT ATTTTAATCT CTCTAAACAT ATTGAAGTTT  
 9651 TAGGGCCCTA AGGAACCTTA GTGATCTTCT ATTGGGTCTT TCTGAGGTT  
 9701 AGAGAGGGTA AGTAACCTCC TCCAGGTAC ACAGCAAGTC TGTGGGTGGC  
 9751 AGAAGCAAGC TAGCGCTGGG CATTCACTAC ATACCACGAT GTGCTCCCTC  
 9801 TCTTGATGCT TGGCCCCCTGG GCCCTTCAGG GCTTGGGAC ATCTTGTCT  
 9851 CAACCCCTCTC CCTAGATCAG TCTGTGAGGG TCCCTGTAGA TATTGTGTAC  
 9901 ACCATGCCCA TGTTATACAG AGTACACACA GATGTACACA CAGATGTACA  
 9951 CATGCTCCAG CCCAGCTCT GCATACCTGC ACCTGCACCC CAGCCTTGGC  
 10001 CCCTGCCTGC GTCTGTGCTC AAAGCAGCAG CTCCAACCCT GCCTCTGTCC  
 10051 CCTTCCCCAC CCACTGCCTG AGCCTTCTGA GCAGACCAGG TACCTTGGCT  
 10101 GCACCGGTGT GTGGCCCGCT CTCACCCAGG CACAGCCCCG CCACCATGGA  
 10151 TCTCCGTGTA CACTATCAAT AAAAGTGGGT TTGTTACAAA GCCGTGTCC  
 10201 TGCCCAGTGT TATTTTTGT ATTTCCAAGA GGAGGTGTGC CCCTTTCCAG  
 10251 ACCAAAGCTG GCCTTCCCT CCCAAATGAC ACCTGCCGTG TACCTTGGCC  
 10301 CTGAGGGTCA GCACTGAGTC CACCTTCAAG TGTAAGTGTG GGGAGAGGG  
 10351 GATAAGTCCC CCAGATGGAA GGTGATGCC TCCTTCAGCC TGGCCCTCCT  
 10401 GGGTCCTCCG GGTGTGTGTA CCGAGGTGTC TGTGTCCACA AAGAAGGGC  
 10451 CCCCGTGGAC CATTAGCTCC AGGAGGATCT CCGTGTCTGA GTTCTTTGTG  
 10501 ATTCCTGTAC AGCAGCAATT TCACCCCGAG GGGACAGTTG GCAATCTCTG  
 10551 GAAACCTTT CCAAGCCTGG GGCTGGGGCT GCTACTCTCA TCTGGTGGGT  
 10601 GGAGGCCAGG GACACCATTG AGTATCCTCC AACGCACAGG ATGCCCTC  
 10651 ACCCCCCACCC CACTGAGAAT TATCTGGCT CAAATGCCA GCGTGGGCAG  
 10701 CCTTACTTAG ACTCACCCCA GGGGCTGGGA CACGCCCTCA CCTGCCTGTG  
 10751 ATGGATTGTG TGGACACAT TCTGGACGGA ACCCACAGCA TAAGCACTCC  
 10801 TGTGAAGTGA GACAGGATGT GGGTGAGGAT GGAAAGTGGA GGCTGAGGG  
 10851 GAAGGTCCTGG GCCCTGACCA ACACGGAATG TGCCCCCTGG GACTGAGAGG  
 10901 CTTCCCTGGG CAGAGGGAAA GGAGGAAGTC AGTGAAGTAA AATACTCC  
 10951 GTGTGTTTA CCCAGCAGT CTCACGCCAT CCTATCACCC AGCCCCGAGG  
 11001 GAAGCCCACT CATGTTCACCC CCATCTGAGC ATTTAGGCTC AGAGAGCTCA  
 11051 ATATCTTGTCA CAAGATGGCA CAGCTGGTGA AGTGGCAGAT CAGAGATTCA  
 11101 ACACCAGAGG CTGTCGATT TCCGTCTGGC TGAAGAAAGA TTTTGCATCA  
 11151 GGGAGGTGGA AACCATCTGT GCTTTTGATC AGCAAATGCC ACCAGCAGGA  
 11201 TCAGGGAGCC AGGCCATAAA G

#### FEATURES:

Start: 3000  
 Exon: 3000-3270  
 Intron: 3271-7693  
 Exon: 7694-8220  
 Stop: 8221

#### CHROMOSOME MAP POSITION:

Chromosome 22

#### ALLELIC VARIANTS (SNPs):

DNA	Position	Major	Minor	Domain
	3951	C	T	Intron
	4127	C	T	Intron
	4157	G	A	Intron
	4513	C	T	Intron
	6894	C	A	Intron
	8409	G	C	Beyond ORF(3')
	8437	T	G	Beyond ORF(3')
	8579	T	C	Beyond ORF(3')
	10292	A	G	Beyond ORF(3')
	10792	A	G	Beyond ORF(3')

Context:

DNA Position	
3951	CACACCCCAGGCCCTTGCACACCTCTAGAGAGGTAAGGGCAGGACCCAGGCAGTGATCAC CAAAGGGAAAGGGGGCTTGGTCATGGTCATAGTGATGGTGATGGCACTAGCTGACACTTAT CAGAAGCTATGGGCCTGGCCCTGTTCTAGAGCTGGCATGTAGTTTTTTGAAACAGA GTCTCGCTCTGTCACCCAGGCTGGAGTCAGTGGCGCATCTCGGCTCACTGCAACCTCT GCCTCCGGGTTCAAGCGATTCTCCTGCCTCAGTCCCCAAGTAGCTGGACTACAGGCA [C, T] GTGCCACCATGCCGGCTAATTTTGATTTTACTAGAGACGGGATTTACCATGTTA GCCAGGATGGTCTCGATCTCTGACCTCGTGAATCTGCTAACCTCAGCCTCCCAAAGTGCT GAGATTACAGGCGTCAGCCACCGCGGCCAGCCAGCATGTAGTTATTTAACCCCTCACAGTA AATAGTTATTCAATTCCCTTTACAGGTGGGAAACTGAAGCCCAGAGAGGTTAAGTAAC TCACTCCAGTGGTAGCACAGCTGTAAAGGCAGTCGCTTTGTGCTTTCAAGACAAAGCC [C, T] CAGAGTCTCGCTCTGTCACCCAGGCTGGAGTCAGTGGCGCATCTGGCTCACTGCAAC CTCTGCCTCCGGGTTCAAGCGATTCTCCTGCCTCAGTCCCCAAGTAGCTGGACTACAA GGCACGTGCCACCATGCCGGCTAATTTTGATTTTACTAGAGACGGGATTTACCA TGTTAGCCAGGATGGTCTCGATCTCCTGACCTCGTGAATCTGCTTACCTCAGCCTCCCAA GTGCTGAGATTACAGGCGTCAGCCACCGCGGCCAGCCAGCATGTAGTTATTTAACCCCTCA [C, T] AGTAAATAGTTATTCAATTCCCTTTACAGGTGGGAAACTGAAGCCCAGAGAGGTTAAG TAACACTCCAGTGGTAGCACAGCTGTAAAGGCAGTCGCTTTGTGCTTTCAAGACAA AGCCATACCACAGCCTCTAGCCCTGCTGGAGGGTGAAGGAGGGACAGGGAGGTTGGGG GGAAGAAGGGGTGAGTGGAGCTGAGGGCTGTGCCCTGTTTACACTGCATTAGCATGGT AGCTAAGAGGACAAGCCGGGACCCAGCACCTGGGTGAGCCCTGGTTCCGCTGCTTCC [G, A] TGCACTGGCGCGATCTCGCTCACTGCAACCTCTGCCTCCGGGTTCAAGCGATTCTCCT GCCTCAGTCCCCAAGTAGCTGGACTACAGGCACGTGCCACCATGCCGGCTAATTTT TGTATTTTACTAGAGACGGGATTTCACCATGTTAGCCAGGATGGTCTCGATCTCCTGAC CTCGTGAATCTGCTTACCTCAGCCTCCCAAAGTGCTGAGATTACAGGCGTCAGCCACCGCG GCCAGCCAGCATGTAGTTATTTAACCCTCACAGTAAATAGTTATTCAATTCCCTTTACA [G, A] GTGGGGAAACTGAAGCCCAGAGAGGTTAAGTAACTCACTCCAGTGGTAGCACAGCTCGTA AAAGCAGTCTGCTTTGTGCTTTCAAGACAAAGCCATACCCACAGCCTCTAGCCCTGCTGG GAAGGGTGAGGAGGGACAGGGAGGTTGGGGGAAGAAGGGGTGAGTGGAGCTGAGGGCT GTGCCCTGTTTACACTGCATTAGCATGGTAGCTAAGAGGACAAGCCCAGCAC CTGGGTGTGAGCCCTGGTTCCGCTGCTTCTGGCTTGTACCTCGAGGCAAGGGATTTA [C, T] TCGTAAAGCAGTCTGCTTTGTGCTTCAAGACAAAGCCATACCCACAGCCTCTCAGCCCT GCTGGGAAGGGTGAGGAGGGACAGGGAGGTTGGGGGAAGAAGGGGTGAGTGGAGCTGAG GGGCTGTGCCCTGTTTACACTGCATTAGCATGGTAGCTAAGAGGACAAGCCCAGCAC ACCACCTGGGTGTGAGCCCTGGTCCGCTGCTTCTGGCTTGTACCTCGAGGCAAGGG TTTATCTCCTGTGTCAGCACTCTCATCTGTAAGACTGCACCACATCAACACTCATC [C, T] TAAAGGGACTGTGAGACTAAATGAATGAATATGTAAGGCCTTGGTGAGCAGATA AAATGCACAATAAAATCCCCAAGTCTCTGTTGAGTCAGCATTGCAAGTGGCCTGCTAC GGGTTACACGATCACTCCAAGTCACGCCCTGAAGTTGCTGAGCAGGGATAAGGGAAAG GAGTGAGCAGGCAACTCTAGGCATATTCAAGATAACCCCCAACTGAGGTACTTCTAT ACAGAGAAACCCATGCCACTCCAGCCCTGCTGCCCTGAGGCAAGACTGAGGCTGC [C, A] GCACTCCAGCCTGGGCCACAGAGAAAGACTCCATCTCAAAAAAAAAAAAAAAA AAGTTTAAGCAAAGTGAGGAAGGTGCTTATTAAGCTGGAAATCAGGATGGAGGTACC AGTCCAGACAGCCTCCCCACCAACCCACCGTCTCCACAGCAGGCCCTGTTCAAGATTCA AAGCCTGCCCTGAGTGATGCAGTGAGTTATCCTGGAGGCAGTGTGGCCTGGAGGCCAG CACTCACTTTTCATCCTATGATTATTTGAGAAGCAGAGACACCTACCCGGTCCCAGG [C, A] ACGAGCTAGGTGAGAACAGAATCAGGTAGAAATCTCAGCCTAGCCACACGGAAAGCTGTG GATCTTGGGCAGGCTGCATACCTTCTGAGCCTCAGTTGCTCACCTGTAATGCAAAGG TAACAAAATCTTGACAGAGGCATAGTGAGGAATCAAGAGAACACACGGGCCCTGGAGC ACCCAGTGCTTAGCCCCAGTAGGCCCTCACTCTCATCATTACTGACACCTGAGGTCACT GAGCATGTGCCACTGTCCATTCTGCATAACTCCCCAAATCATCCTGCAAGGTA
4127	
4157	
4513	
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FIGURE 3, page 5 of 6

8409	CATGGTCTGCCCTTCGCCGCCGCCAGCGTCAACAGTGACCTCAAGTACATCAAGGC CAAGGTCTCGGAAGGCCAGGCCCCGTGAGAGGGACAAGTGCACCATCCAGTGAGCGAG GGATGCTGGGGGGCTTGGCCAGTGCCTCAGGGAGGTGGCCCCAGATGCCACTGTG CGCATCTCCCACCGAGGCCCGCAGCAGTCTTGTACAGACCTTAGGCACCAGACTG GAGGCCCGGGCGCTGGCTCCGCACATTGTCTGCCTCTCACAGCTTCAGTCC [G, C] CTTGTCCACAGCTCCGTGGGTTTCATCTCCTCTGTGGGAGGACACATCTCTGCAGCCT CAAGAGTTAGGCAGAGACTCAAGTTACACCTTCCTCTCTGGGGTTGGAAGAAATGTTGA TGCAGAGGGGTGAGGATTGCTGCGTCATATGGAGCCTCTGGGACAAGCCTCAGGATGA AAAGGACACAGAAGGCCAGATGAGAAAGGTCTCTCTCTGGCATAAACACCCAGCTTG GTTGGGTGGCAGCTGGGAGAACTTCTCTCCAGCCCTGCAACTCTTACGCTCTGGTTCA
8437	AGCGTCAACAGTGACCTCAAGTACATCAAGGCCAGGTCTCGGAAGGCCAGGCC GAGAGGGACAAGTGCACCATCCAGTGAGCGAGGGATGCTGGGGGGCTTGGCCAGTGC CTTCAGGGAGGTGGCCCCAGATGCCACTGTGCGCATCTCCCCACCGAGGCCCGGCAGC AGTCTTGTACAGACCTTAGGCACCAAGACTGGAGGCCGGCGCTGGCTCCGCACA TTCGTCTGCCTCTCACAGCTTCTGTAGTCAGCTGAGTCCACAGCTCTGGTGGTTCA [T, G] CTCCTCTGTGGGAGGACACATCTCGAGCCTCAAGAGTTAGGCAGAGACTCAAGTACA CCTCCTCTCTGGGGTTGGAAGAAATGTTGATGCCAGAGGGGTGAGGATTGCTGCTGCA TATGGAGCCTCTGGGACAAGCCTCAGGATGAAAAGGACACAGAAGGCCAGATGAGAAAG GTCTCCTCTCTCTGGCATAAACACCCAGCTTGGTTGGGTGGCAGCTGGGAGACTTC TCCCAGCCCTGCAACTCTTACGCTCTGGTTCAAGCTGCCCTGACCCCCCTCCCACCCCCA
8579	GCCCACGTGCGCATCTCCCCACCGAGGCCGGCAGCAGTCTTGTACAGACCTTAGG CACCAAGACTGGAGGCCGGCGCTGGCTCCGCACATTGCTGCTGCCCTCTCACAGCTT TCCTGAGTCCGCTTGTCCACAGCTCTTGTGGTTCATCTCTCTGTGGGAGGACACAT CTCTGCAGCCTCAAGAGTTAGGCAGAGACTCAAGTTACACCTTCCTCTGGGGTTGGA AGAAATGTTGATGCCAGAGGGGTGAGGATTGCTGCGTCATATGGAGCCTCTGGGACAAG [T, C] CTCAGGATGAAAAGGACACAGAAGGCCAGATGAGAAAGGTCTCTCTCTCTGGCATAAC ACCCAGCTGGTTGGGTGGCAGCTGGGAGAACTCTCTCCAGCCCTGCAACTCTTACG CTCTGGTTAGCTGCCCTGACACCCCCCTCCACACACACAAGTTGGGCCCC AGCTGCCCTGACATTGAGCCAGTGGACTCTGTGTCTGAAGGGGGCGTGGCCACACCTCC TAGACCACGCCACCACTAGACCACGCCACCTCTGACCGCGTCTCAGCCTCTCT
10292	ACCCCTGGCCCTGCCGTGCTGTGCTCAAAGCAGCAGCTCCAACCCCTGCCCTGTCCC CTTCCCCACCCACTGCCGTGAGCCTCTGAGCAGACCCAGGTACCTGGCTGCACCGGTGTG TGGCCCGCTCTCACCCAGGCACAGGCCACCATGGATCTCGTGTACACTATCAATA AAAGTGGTTGTTACAAGCCGTCTTGCCTGCCATGTGTATTTTGATTTCCAAGAG GAGGTGTGCCCTTCCAGACCAAAGCTGCCCTTCCCAAATGCACCTGCCGTGT [A, G] CCCTGGCCCTGAGGGTCAGCACTGAGTCCACCTCAAGTGTAAAGTGTGGGAGAGGGG TAAGTCCCCAGATGGAAGGTGATGCCCTCTCAGCCTGGCCCTCTGGGTCTCCGG TGTGTGTACCGAGGTGTCGTGTCCACAAAGAAGGGGCCCGTGGACCATTAGCTCCAG GAGGATCTCGTGTCTGAGTTCTTGATTCCTGTACAGCAGCAATTCAACCGCAGGG GACAGTTGGCAATCTTGAAACCTTCCAAGCTGGGCTGGGCTGCTACTCTCATC
10792	TTCTTTGTGATTCTGTACAGCAGCAATTCAACCCGAGGGGACAGTGGCAATCTCTGG AAACCTTTCCAAGCCTGGGCTGGGCTGCTACTCTCATCTGGGGTGGAGGCCAGGG ACACCAATTCAAGTCTCCAACGCACAGGATGCCCTCCACCCCCACCCACTGAGAATT ATCTGGCCTCAAATGCCAACCGTGGCAGCCTTACTTAGACTCACCCAGGGCTGGGAC ACGCCACCTGCGTGTGATGGATTGTTGGACACATTCTGGACGGAACCCACAGCAT [A, G] AGCACTCCTGTGAAGTGTGAGACAGGATGTGGGTGAGGATGGAAGTGGAGGCTGGGGAGA AGGTCTGGCCCTGACCAACACGGAATGTGCCCTCTGGACTGAGAGGCTCCCTGGGCA GAGGGAAAGGAGGAAGTCAGTGAGGTAAGGACTCCCTGTGTGTTTACCCAGCGAGTCT CACGCCATCTTACCCAGCCCGAGGGAAAGCCACTCATGTTCACCCCATCTGAGCAT TTAGGCTCAGAGAGCTAATATCTGTCCAAGATGGCACAGCTGGTAAGTGGCAGATCA

FIGURE 3, page 6 of 6